

1	AGCAGACAGAGGACTCTCATTAAGGAAGG	TGTCCTGTGCCCTGACCCTACAGATGCCA	MetPro	ArgGluaspalaHisPheileTyriGlyTyx	CCCAAGAAGGGGCACGCCCACTCTTACACC	119
22						22
120	ACGCTGAAGAGCGCGTGGATCGGCATC	CTGACAGTGAATCTGGAGTCTTACTGCTC		ATCGGCTGTGGTATTTAGACACGAAAT	GGATACAGAGCCTTGTATGATAAAAGTCTT	239
23	ThrAlaGluGluAlaAlaGluVilledlyla	LeuThrValIleLeuGluValIleuLeuLeu		IleGlyCysPheTyx	GlyTyxArgAlaLeuLeuHisAspLysSerLeu	62
240	CATGTTGGCACTCAATGTGCTTAACAAGA	AGATGCCCAACAAGAGGTTTGATCATCGG		GACAGCAAGGTGCTCTTCAAGAGAAAAAC	TGTGAACCTGTGGTTCCCAATGCTCCACCT	359
63	HisValGlyThrGlnCysAlaLeuThrArg	ArgCysProGlnGluGluPheAspHisArg		AspSerLysValSerLeuGlnGluLysAsn	CysGluProValValProAsnAlaProPro	102
360	GCTTATGAGAACTCTCTGCAGAACAGTCA	CCACCACCTTATTCACCTTAAGAGCCAGCG		AGACACCTGAGACATGCTGAAATTTATTTCT	CTCACACTTTTGTGCTTGAATTTAATACAGAC	479
103	AlaTyrgluLysLeuSerAlaGluGlnSer	ProProProTyxSerPro				118
480	ATCTAATGTTCTCTTGGAAATGGTGAAG	AAAAATGCAAGCCATCTCTAATAATAAGTC		AGTGTAAATTTTGTAGGTCCGCTAGCA	GTAATAATCATGTGAGGAAATGATGAGAAA	599
600	TATTAAATGGGAACCTCCATCAATAAAT	GTGGCAATGCATGATATCTGTGCCAGA		GATTAATGTAGTAATTCATGCTGTTATTT	TCTGAGAGACAGAAATTCAGTGGGTATTTCT	719
720	GGGGCATCCAAATTTCTTTTACTTGAAT	TTGGCTAATAACAATACTAGTCAGGTTTTCG		AACCTTGACCGACATGAACTGTACACAGAA	TTGTTCACGACTATGAGTGTCTCACAAAG	839
840	GATACCTTTACAGGTTAAGACAAGGTTG	ACTGGCTATTTATCTGTATCAAGAACATGT		CAGCAATGTCTCTTGTGCTTAAATTTCT	ATTATACATCAATATATATATTTGTAAGATC	959
960	CTATAGCTCTTTTGTGAGATGGAGTTT	CGCTTTTGTGCGCAGGCTGGAGTGCATG		GCGGATCTTGGCTCACCATAACTCCGCGCC	TCCCAGGTTCAAGCAATTTCTCTGCTTAG	1079
1080	TCTGCCGCTCAGCTCCCAAGTCTGCTGG	AAATPACAGCGCTGAGCCACCGCTGGCT		GAATCCTATATCTTAGGTAAAGACATATAAC	GCACTCTAATTTACATTTCTACTCAAGGCTC	1199
1200	ATGCTATTCTTAATGACAAAGTATTTT	CTACTAAACCAAGAAATTTGGTAGAAGGATTT		AAATAAGTAAAGCTACTATGTACTGCTT	AGTGTGATGCTGTGCTACTGCTTAAATG	1319
1440	TACCTATGGCAATTTAGCTCTCTTGGGTC	CCAAATCCCTCTCTCAAGAATGTGCAGAG		AAATCATAAAGGATCAGAGATTTCTGAATA	AAAAAAAATAAAAAATAAAAAATAAAAA	1559

FIGURE 1

A42

Peptide concentration (ug/ml)	% specific lysis (●)	% specific lysis (▼)	% specific lysis (■)
0.00001	0	0	0
0.0001	2	0	0
0.001	25	2	2
0.01	75	5	2
0.1	90	22	3
1	78	52	1
10	77	58	3

TIL1235

Peptide concentration (ug/ml)	% specific lysis (●)	% specific lysis (▼)	% specific lysis (■)
0.00001	2	1	1
0.0001	5	10	2
0.001	10	12	3
0.01	18	10	5
0.1	38	22	5
1	65	42	5
10	90	75	4

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GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GSTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGA CTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG	720
GGAACAAGCA CTTCTGAGA AATCAGCCTC TGACCTTTGC	760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT	800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA	840
CCCTGATCTC TCGGGCACTT GTGGTCACTC AACTTACCT	880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT	920
GCCATTCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG	960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCTAA	1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT	1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA	1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC	1120

FIGURE 4

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIGURE 4 (continued)

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FIGURE 5A

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1 MDLVLRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRLR TKAWNRLYP
51 EWTEAQLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG
101 QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151 YVWKTWQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSTY
251 LAEADLSYTW DFGDSSGTLI SRALVVHTY LEPGPVTAQV VLQAAIPLTS
301 CGSSPVP GTT DGHRTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451 TGSIGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501 AVPSGEGDAF ELTVSCQGL PKEACMEISS PGCQPPAQL CQVLPSPAC
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601 GILLVLMVAV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651 ENSPLLSGQQ V

```

FIGURE 5B

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Pme117 M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20 M-----V-----Q-----L-----
gp100 M-----V-----Q-----L-----
cDNA25FL M-----F-----Q-----L-----
cDNA25TR Q-----L-----PPQWAAGLSTLI
1 162 236 274 588 649

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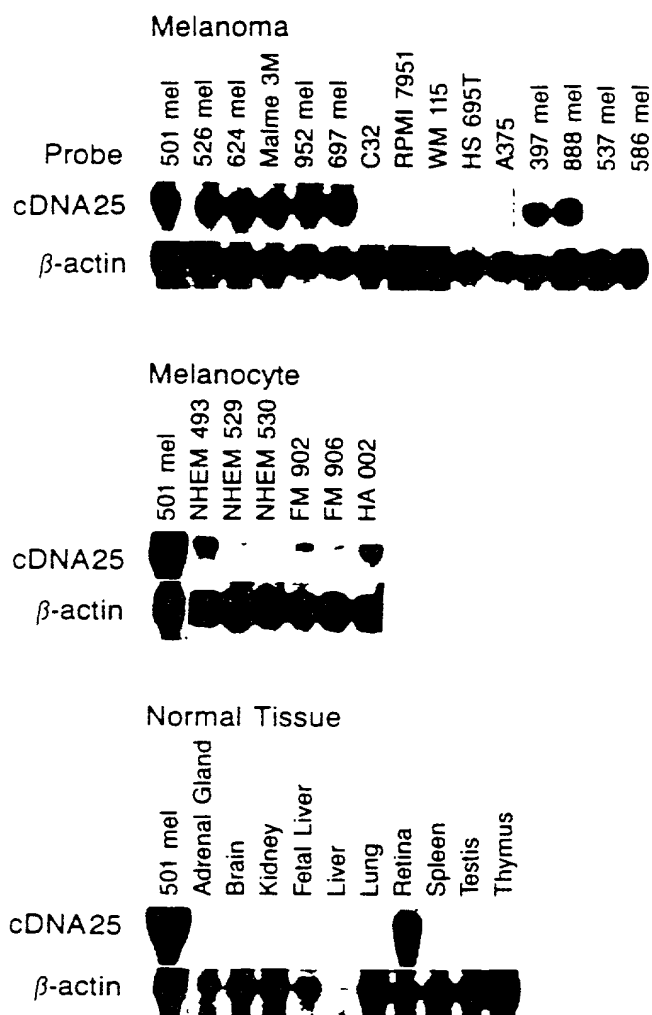


FIGURE 6